BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/810,861_

Source: _OIPE_

Date Processed by STIC: _3/30/2001_

Checker Version 3.0

Checker Version 3.0 can be downloaded from the USPTO website at the following:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION

SERIAL NUMBER: 09/810,861

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/05/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/810,861

DATE: 03/30/2001
TIME: 14:45:03

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Output Set: N:\CRF3\03302001\I810861.raw

Does Not Comply
Corrected Diskette Needed

p.6

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 4         Soreq, Hermona
 5         Arntzen, Charles J.
 6         Mason, Hugh S.
 8 <120> TITLE OF INVENTION: EXPRESSION OF RECOMBINANT HUMAN ACETYLCHOLINESTERASE IN
 9         TRANSGENIC PLANTS
11 <130> FILE REFERENCE: BTI-45
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C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/810,861
C--> 14 <141> CURRENT FILING DATE: 2001-03-16
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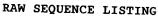
RAW SEQUENCE LISTING   DATE: 03/30/2001
PATENT APPLICATION: US/09/810,861   TIME: 14:45:03

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Output Set: N:\CRF3\03302001\I810861.raw

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/810,861

DATE: 03/30/2001
TIME: 14:45:03

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Output Set: N:\CRF3\03302001\I810861.raw

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233 acagcagagc catgtagaca acatcccctc cccctttcca ccgcgtcaga cgcccgtagc 3840
234 agcccgctac gggctttttc atgccctgcc ctagcgtcca agcctcacgg ccgcgctcgg 3900
235 cctctctggc ggccttctgg cgctcttccg cttcctcgct cactgactcg ctgcgctcgg 3960
236 tcgttcggct gcggcgagcg gtatcagctc actcaaaggc ggtaatacgg ttatccacag 4020
237 aatcagggga taacgcagga aagaacatgt gagcaaaagg ccagcaaaag gccaggaacc 4080
238 gtaaaaaggc cgcgttgctg gcgtttttcc ataggctccg cccccctgac gagcatcaca 4140
239 aaaatcgacg ctcaagtcag aggtggcgaa acccgacagg actataaaga taccaggcgt 4200
240 ttccccctgg aagctccctc gtgcgctctc ctgttccgac cctgccgctt accggatacc 4260
241 tgtccgcctt tctcccttcg ggaagcgtgg cgctttccg ctgcataacc ctgcttcggg 4320
242 gtcattatag cgattttttc ggtatatcca tcctttttcg cacgatatac aggattttgc 4380
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245 gtgctcaacg ggaatcctgc tctgcgaggc tggccggcta ccgccggcgt aacagatgag 4560
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247 tactgccttc cagacgaacg aagagcgatt gaggaaaagg cggcggcggc cggcatgagc 4680
248 ctgtcggcct acctgctggc cgtcggccag ggctacaaaa tcacgggcgt cgtggactat 4740
249 gagcacgtcc gcgagctggc ccgcatcaat ggcgacctgg ccgcctggg cggcctgctg 4800
250 aaactctggc tcaccgacga cccgcgcacg gcgcggttcg gtgatgccac gatcctcgcc 4860
251 ctgctggcga agatcgaaga gaagcaggac gagcttggca aggtcatgat gggcgtggtc 4920
252 cgcccgaggg cagagccatg acttttttag ccgctaaaac ggccggggg tgcgcgtgat 4980
253 tgccaagcac gtccccatgc gctccatcaa gaagagcgac ttcgcggagc tggtgaagta 5040
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256 cgtgtgcgag acaccgcggc cgccggcgtt gtggatacct cgcggaaaac ttggccctca 5220
257 ctgacagatg aggggcggac gttgacactt gagggggccga ctcacccggc gcggcgttga 5280
258 cagatgaggg gcaggctcga tttcggccgg cgacgtggag ctggccagcc tcgcaaatcg 5340
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265 cggcccgcta acgcgggcct cccatccccc cagggctgc gcccctcggc cgcgaacggc 5760
266 ctcaccccaa aaatggcagc gctggcagtc cttgccattg ccgggatcgg ggcagtaacg 5820
```

```
ttttcccagt cacgacgttg taaaacgacg gccagtgaat tnnnnnnnnn nnnnnnnnnn 11880
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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnngga tccagatccc gtgggcgaag 12180
```

see item 10 on Error Summary Sheet

Input Set : **A:\Bti45sel.app**
Output Set: **N:\CRF3\03302001\I810861.raw**

```
L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:367 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:367 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:368 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:368 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:369 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:369 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:369 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:370 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:370 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:370 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:371 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:371 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:372 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:372 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:372 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
```